CLAIMS

What is claimed is:

1. A method for identifying a microorganism, comprising the following steps (1) to (5):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of the sequence pairs (69) and (74), (69) and (78), (72) and (71), (72) and (74), and (72) and (78);

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) isolating said DNA fragment;

(4) determining the nucleotide sequence of said DNA fragment; and

(5) identifying the microorganism by comparing the sequence of the amplified *gyrB* gene DNA fragment to known *gyrB* gene DNA fragment sequences.

2. The method for identifying a microorganism according to claim 1, wherein the amino acid sequence pairs that are used are sequence pairs (69) and (74), (69) and (78), (72) and (74), or (72) and (78); and said microorganism belongs to *proteobacteria*.

3. A method for identifying a microorganism, comprising the following steps (1) to (8):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences (69) and (71);

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of amino acid sequences (69) and (73);

(4) synthesizing forward and reverse primers based on a single pair of amino acid sequences (70) and (71);

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) identifying the microorganism by comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

4. A method for identifying a microorganism, comprising the following steps (1) to (8):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences (69) and (74);

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of amino acid sequences (69) and (73);

(4) synthesizing forward and reverse primers based on a single pair of amino acid sequences (70) and (74);

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) identifying the microorganism by comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

5. A method for identifying a microorganism, comprising the following steps (1) to (8):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences (72) and (74);

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to

produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of amino acid sequences (72) and (73);

(4) synthesizing forward and reverse primers based on a single pair of amino acid sequences (70) and (74);

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) identifying the microorganism by comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

6. A method for identifying a microorganism, comprising the following steps (1) to (6):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences (72) and (73);

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of (76) and (71), (76) and (74), or (76) and (75);

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) identifying the microorganism by comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

7. A method for identifying a microorganism, comprising the following steps (1) to (6):

(1) synthesizing forward and reverse primers based on a single pair of amino acid

sequences (69) and (77);

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of (79) and (71), (79) and (74), or (79) and (75);

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) identifying the microorganism by comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

8. A method for identifying a microorganism, comprising the following steps (1) to (6):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences (69) and (77);

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of (80) and (71), (80) and (74), or (80) and (75);

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) identifying the microorganism by comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

9. A method for detecting a microorganism, comprising the following steps (1) to (5):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of the sequence pairs (69) and (74), (69)

and (78), (72) and (71), (72) and (74), and (72) and (78);

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) isolating said DNA fragment;

(4) determining the nucleotide sequence of said DNA fragment; and

(5) detecting the microorganism by comparing the nucleotide sequence of said amplified *gyrB* gene DNA fragment to known *gyrB* gene DNA fragment sequences.

10. The method for detecting a microorganism according to claim 9, wherein the amino acid sequence pairs that are used are sequence pairs (69) and (74), (69) and (78), (72) and (74), or (72) and (78); and said microorganism belongs to *proteobacteria*.

11. A method for detecting a microorganism, comprising the following steps (1) to (8):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences (69) and (71);

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of amino acid sequences (69) and (73);

(4) synthesizing forward and reverse primers based on a single pair of amino acid sequences (70) and (71);

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two primers to produce two *gyrB* gene DNA fragments;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) detecting the microorganism by comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

12. A method for detecting a microorganism, comprising the following steps (1) to (8):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences (69) and (74);

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of amino acid sequences (69) and (73);

(4) synthesizing forward and reverse primers based on a single pair of amino acid sequences (70) and (74);

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) detecting the microorganism by comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

13. A method for detecting a microorganism, comprising the following steps (1) to (8):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences (72) and (74);

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of amino acid sequences (72) and (73);

(4) synthesizing forward and reverse primers based on a single pair of amino acid sequences (70) and (74);

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) detecting the microorganism by comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

14. A method for detecting a microorganism, comprising the following steps (1) to (6):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences (72) and (73);

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of (76) and (71), (76) and (74), or (76) and (75);

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) detecting the microorganism by comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

15. A method for detecting a microorganism, comprising the following steps (1) to (6):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences (69) and (77);

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of (79) and (71), (79) and (74), or (79) and (75);

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) detecting the microorganism by comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

16. A method for detecting a microorganism, comprising the following steps (1) to (6):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences (69) and (77);

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of (80) and (71), (80) and (74), or (80) and (75);

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) detecting the microorganism by comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.